

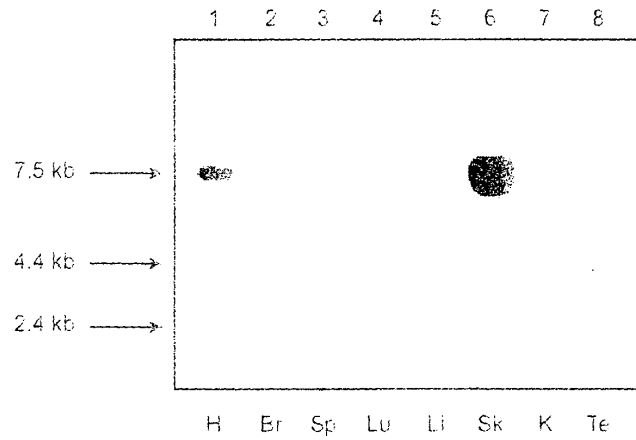
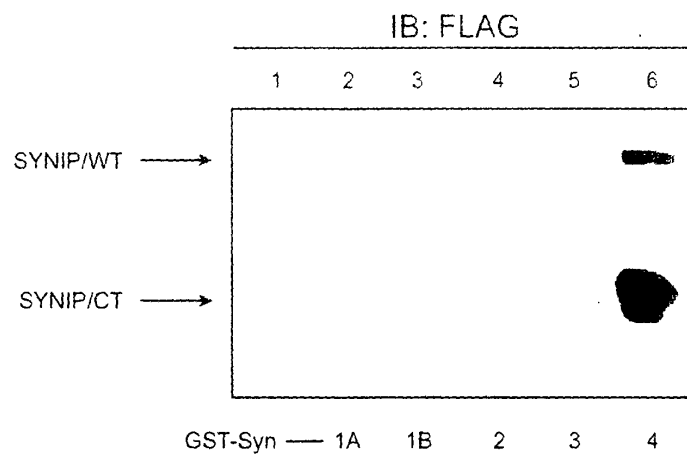
# FIG-1A SYNIP AMINO ACID SEQUENCE

1 MSDGTASARS SSPLD RDPAF RVITVTKETG LGIKILGGIN RNEGPLYVIH EVIPGGDCYK DGR LKPGDQL 70  
 71 VSINKESMIG VSEEEAKSII TRAKLRSESP WEIAFIROKS YCGHPGNICC PSPQVSEDCG POTSTFTLLS 140  
 141 SPSETLLPKT SSTPQTQDST FPSCKAIQTK PEHDKTEHSP ITS LDNSPAD TSNADIAPAW TDDDSGPQ GK 210  
 211 ISLNPSVRLK AEKLEMAINY LGIOPTKEQR EALREQVQAD SKGTVSFGDF VQVARS L FCL QLDEVNVGVH 280  
 281 EIPSILDSQL LPCDSLEADE VGKLRQERNA ALEERNVLKE KLESEKHRK QLIEELQNVK QEAKAVAEET 350  
 351 RALRSRIHLA EAAQROAHGM EMDYEEVIRL LEAEVSELKA QLADYSDONK ESVDLRKRV TVLDCQLRKS 420  
 421 EMARKAFKAS TERLLGFIEA IQEVILDSSA PLSTLSERRA VLASQTSIPL LARNGRSFPA TLLLESKELV 490  
 491 RSVRAILDMD CLPYGWEEAY TADGIKYFIN HVTQTTSWIH PVMSALNLSC AESEEDCPR ELTDPKS 557

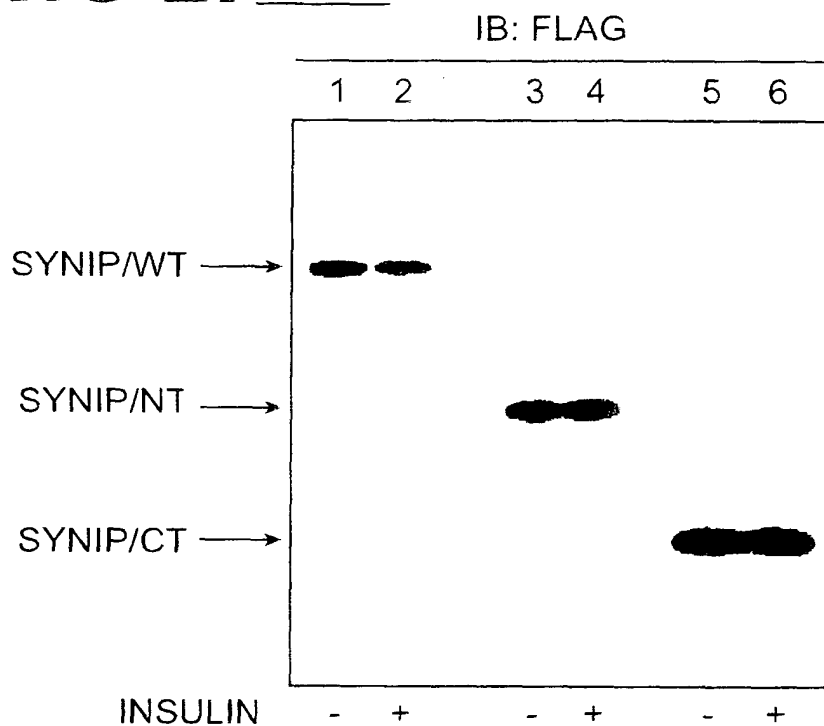
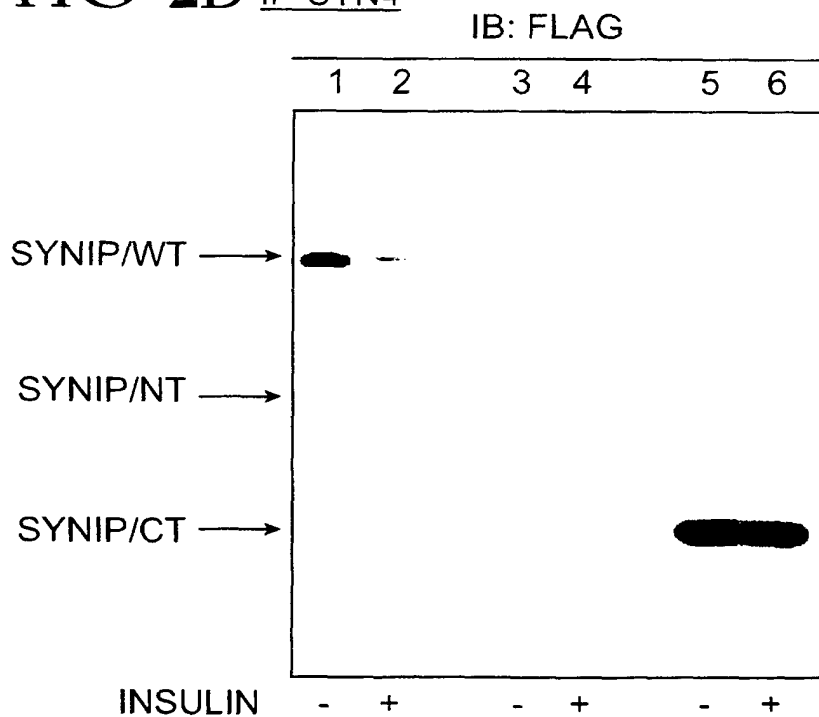
# FIG-1B SYNIP DOMAIN STRUCTURE

19	93	219	264	300	410	500	533
PDZ		EF		CC	CC		WW

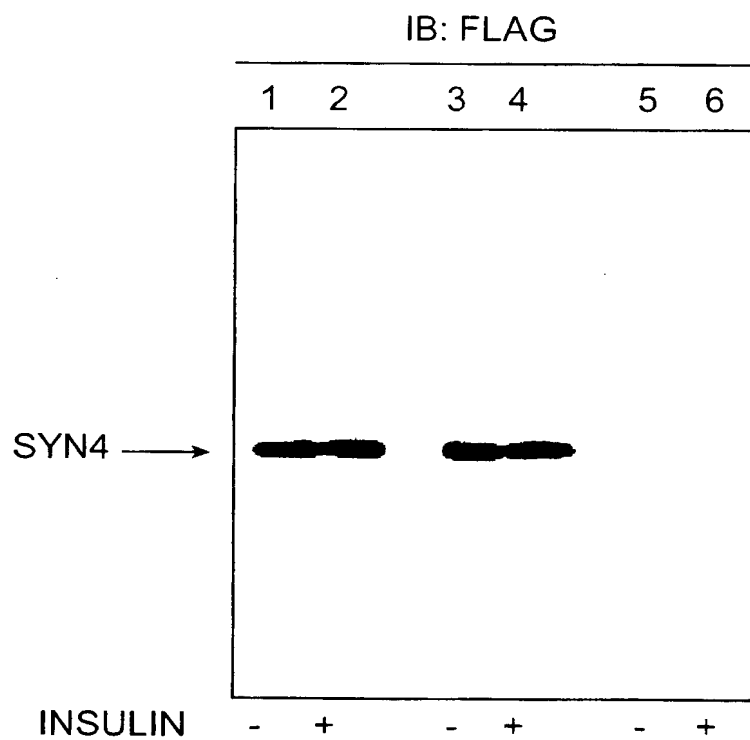
2/12

FIG-1C NORTHERN BLOTFIG-1D BINDING SPECIFICITY

3/12

FIG-2A LYSATEFIG-2B IP-SYN4

4/12

FIG-2C IP-SYN4

5/12

FIG-3A LYSATE

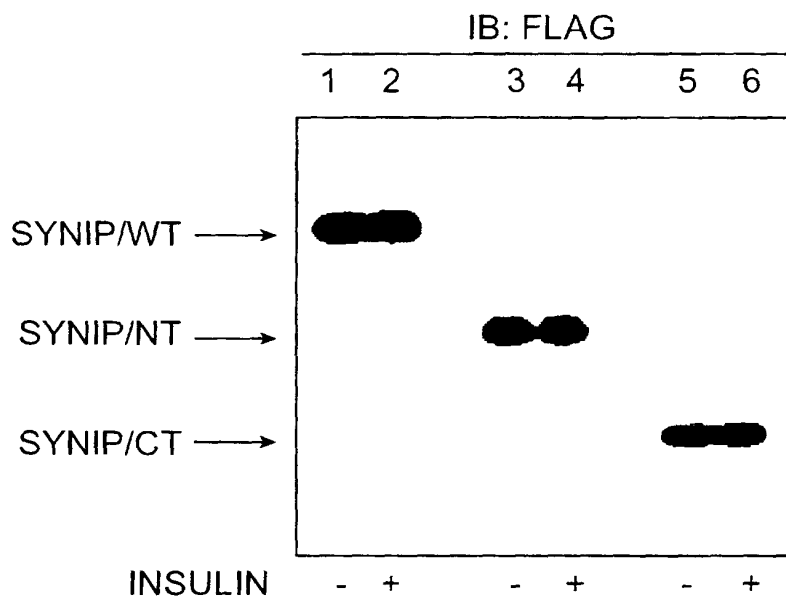
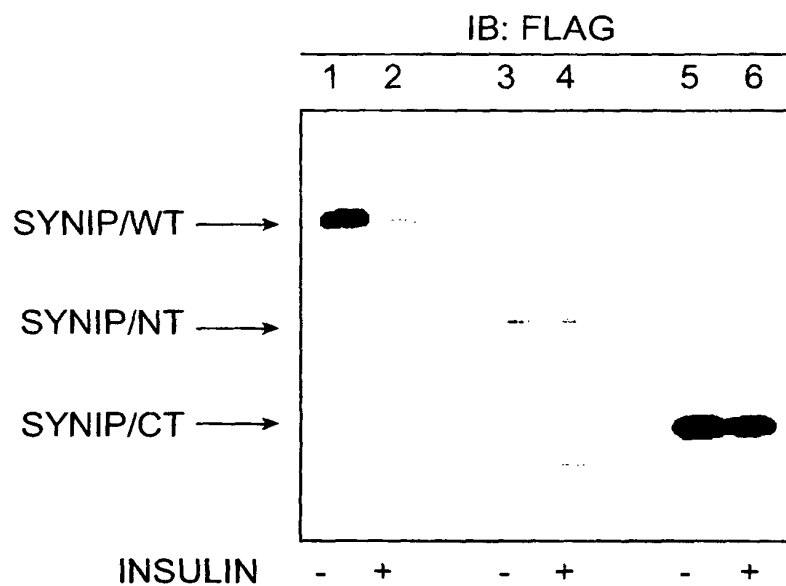
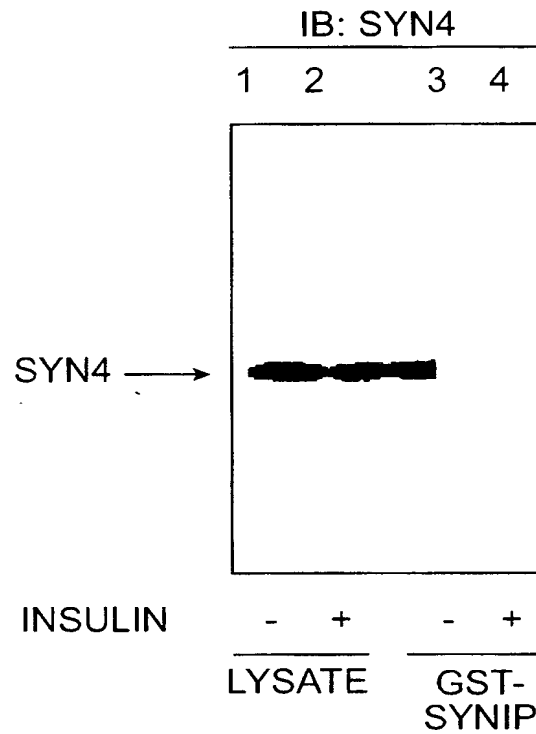
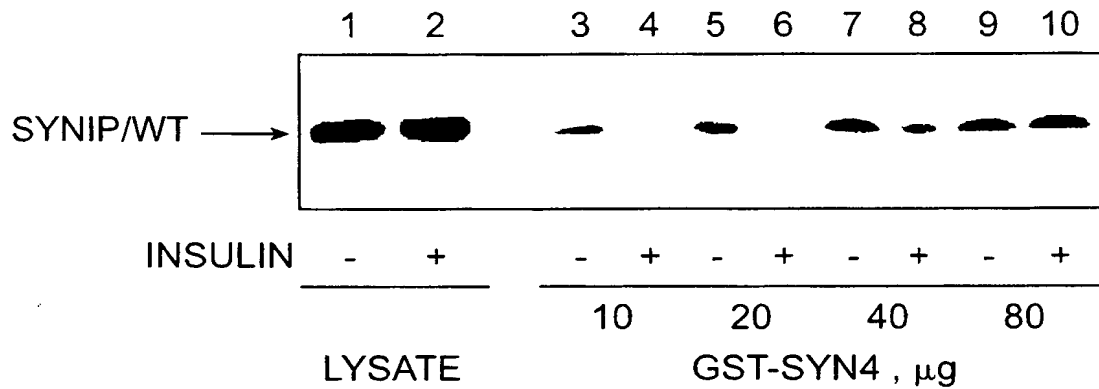


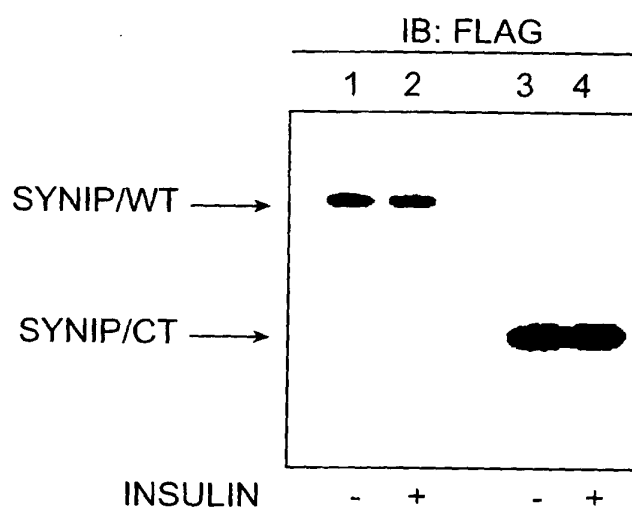
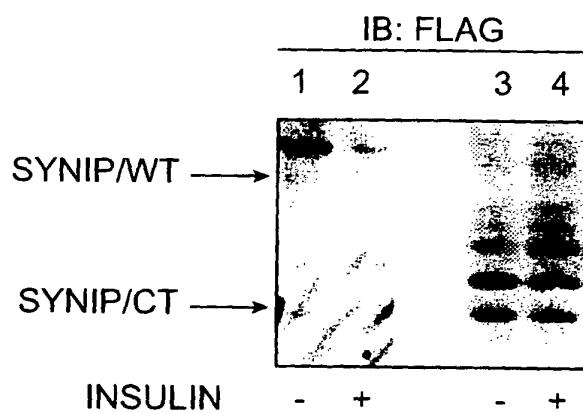
FIG-3B GST-SYN4



6/12

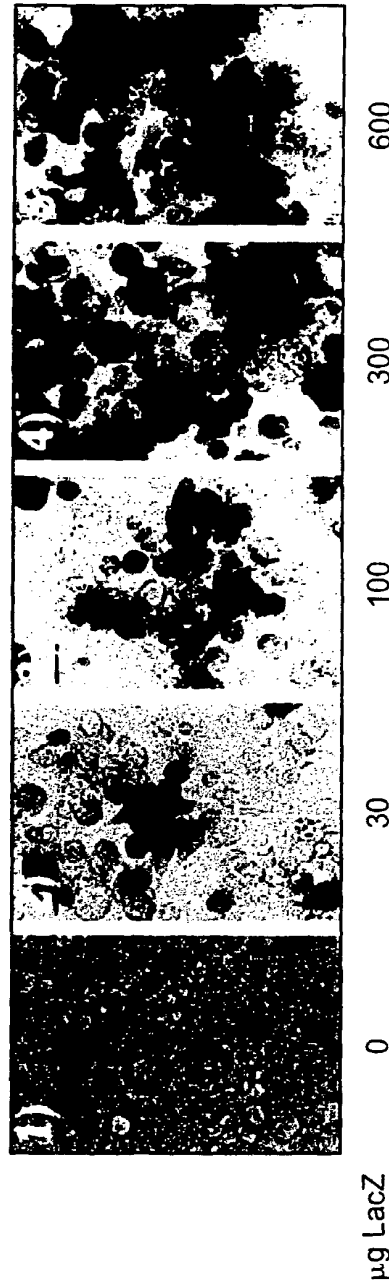
FIG-3C GST-SYNIPFIG-3D IB: FLAG

7/12

FIG-4A LYSATEFIG-4B GST-SYN4

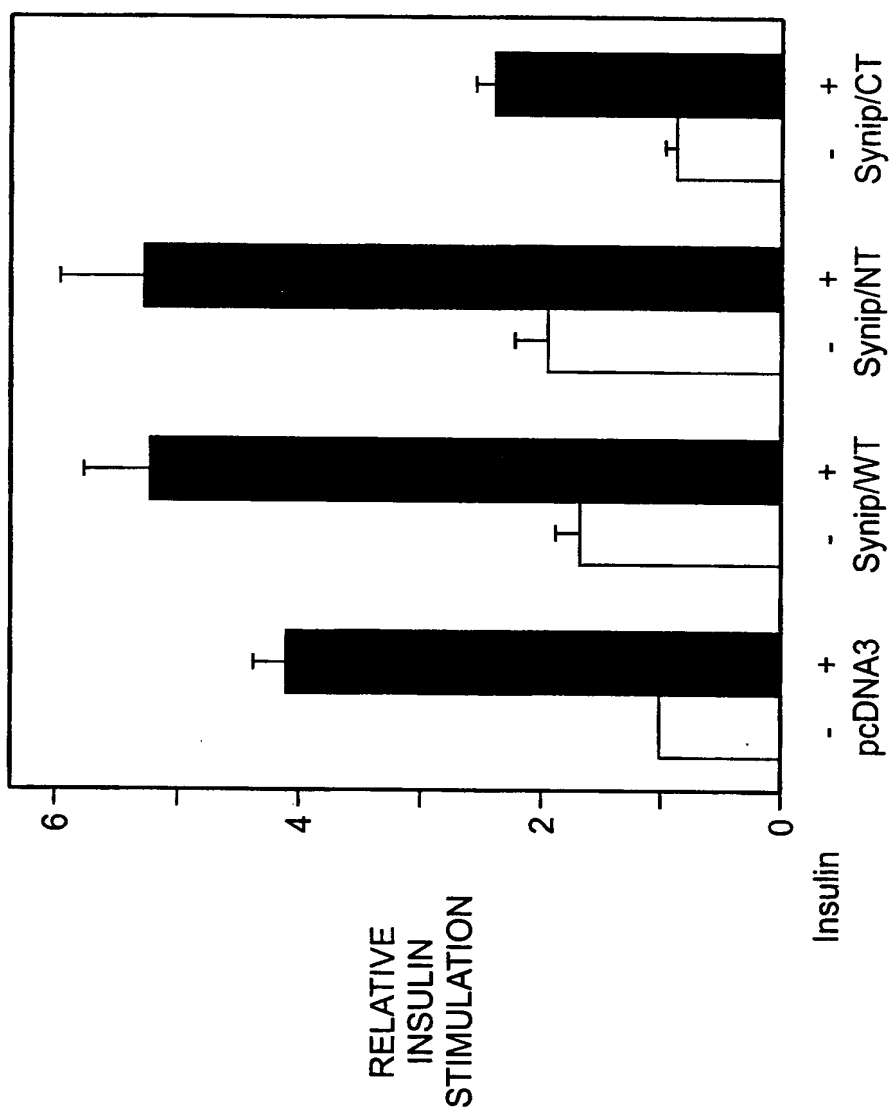
8/12

**FIG-5A**  $\beta$ -GALACTOSIDASE EXPRESSION



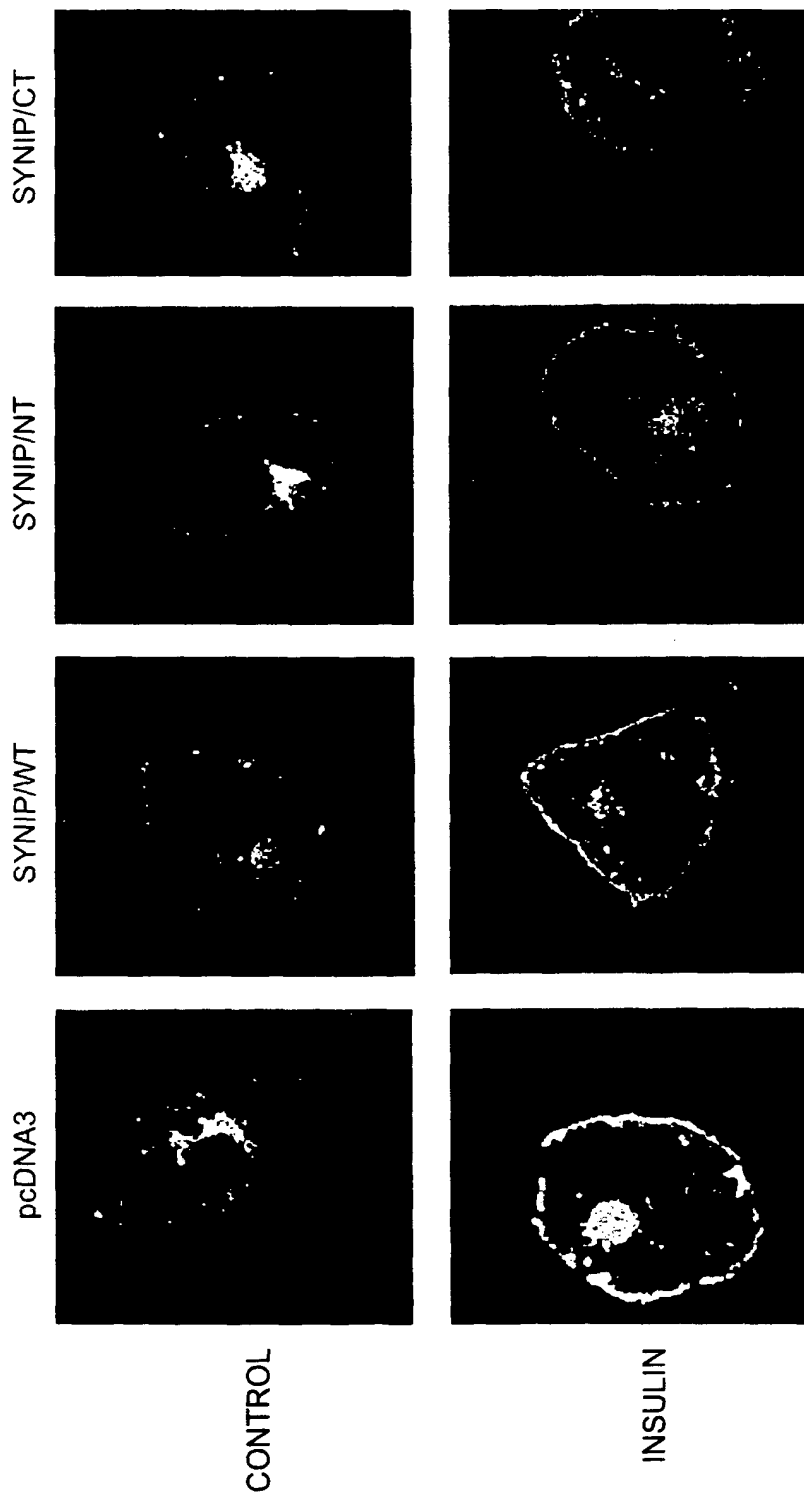
9/12

**FIG-5B** GLUCOSE TRANSPORT



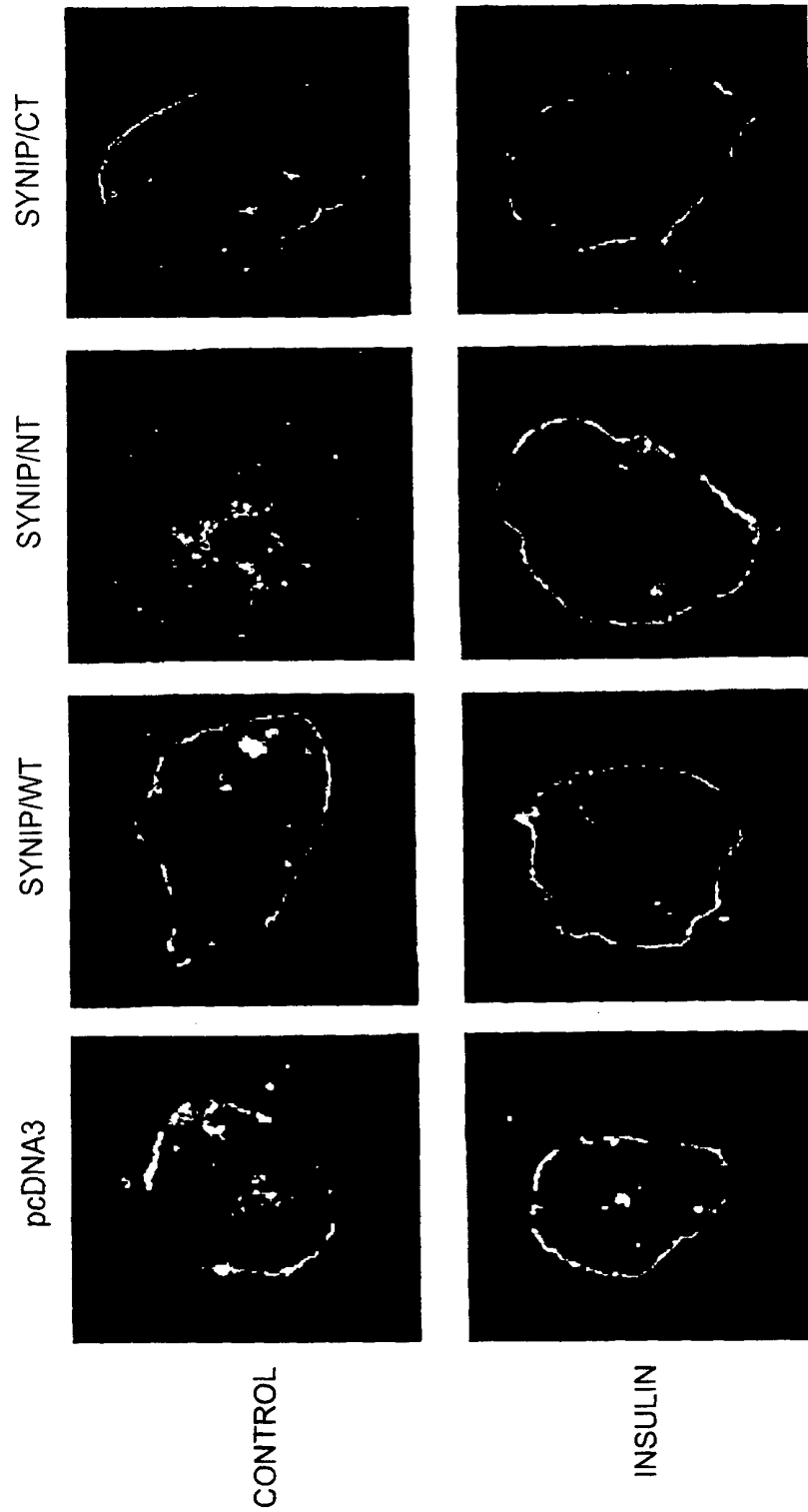
10/12

FIG-6A GLUT4-eGFP



11/12

FIG-6B<sub>eGFP-GLUT1</sub>



12/12

FIG-7

